ABSTRACT

USE OF LINEEAR MODELS WITH NORMAL, STUDENT-t OR SLASH DISTRIBUTED ERROR FOR THE ANALYSIS OF QUANTITATIVE TRAITS

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In this study, multivariate linear mixed effects models with *Normal*, *Student-t* or *Slash* distributed errors were developed to analyze quantitative traits. Five different populations with five replicates were simulated using multivariate linear mixed effects animal models with *Normal* (NOR), three (ST3) or ten (ST10) degrees of freedom *Student-t*, and one and half (ST1.5) or three (SL3) degrees of freedom *Slash* distributed error. In order to validate *Student-t* and *Slash* (Robust) models, each replicate in each population was analyzed to estimate genetic, non-genetic error (co)variances and degrees of freedom using *Normal*, *Student-t* and *Slash* distributed models. Results indicated that unbiased estimate of degrees of freedom for *Normal*, *Student-t* or *Slash* population was obtained from *Student-t* and *Slash* models; and *Student-t* and *Slash* model could be used to fit Normal and heavy-tailed distributed populations. In addition, Predictive Log-Likelihood was found as a good model choice criterion to determine a model fit better for *Normal*, *Student-t* and *Slash* population. Multivariate *Normal*, *Student-t* and *Slash* models were also applied to analyze weaning weight, yearling weight and fleece weight data collected from 12124 Romney sheep in New Zealand. Posterior means of degrees of freedom for *Student-t* and *Slash* models were estimation 12.6 and 3.15. Posterior distributions of direct, maternal genetic and error (co)variances were similar across models. Posterior means of direct and maternal heritabilities from Normal model seemed to agree with those from the *Student-t* and *Slash* models. These results indicate that *Normal*, *Student-t* or *Slash* model is adequate for the analysis of weaning, yearling and fleece weights from Romney sheep.

KeyWords: Robust model, gibbs sampling, *student-t* distribution, *slash* distribution